



AN-2026-00001

Issued 2026-09-22

Certificate of analysis

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Client	Molequa	Report number	AN-2026-00001
Sample	Retatrutide, lyophilised powder, vial labelled 10 mg	Sample received	2026-09-08
Batch number	ATRET-10-2511-01	Date of issue	2026-09-22
Matrix	Research peptide	Determinations performed	18

SUMMARY OF RESULTS

DETERMINATION	METHOD	RESULT	SPECIFICATION
Appearance	Visual	White to off-white powder	White to off-white powder
Identity	LC-HRMS (ESI+), USP <621> principles	Deconvoluted monoisotopic mass 4728.47 Da, deviation 0.4 ppm; observed m/z 1577.16 (3+) and 1183.13 (4+)	Theoretical monoisotopic 4728.472 Da from C221H342N46O68, expected m/z 1577.165 (3+), 1183.125 (4+)
Purity	RP-HPLC, C18, 214 nm, area %	99.23 ± 0.20 % (k = 2)	>= 98.0 %
Related substances	RP-HPLC, 214 nm; LOD 0.01 %, LOQ 0.03 %, reporting threshold 0.05 %	Largest single impurity 0.23 % at RRT 1.03 (± 0.03 %); total impurities 0.77 %, i.e. 0.077 mg per vial	Single <= 1.0 %, total <= 2.0 %
Impurity profile	RP-HPLC with LC-HRMS assignment	RRT 0.93, 0.11 %, -18 Da (Asp succinimide); RRT 0.97, 0.19 %, same mass (isoAsp at Asp9 or Asp15); RRT 1.03, 0.23 %, +0.98 Da (deamidation of Gln3 or Gln18); RRT 1.08, 0.14 %, +16 Da (Tyr oxidation); RRT 1.15, 0.10 %, -18 Da (Asp15 succinimide)	Peaks above 0.05 % reported (ICH Q3B)
Net peptide content	Assay	95.4 ± 1.2 % w/w (k = 2)	—
Fill weight	Gravimetric	10.42 ± 0.05 mg	Labelled 10 mg

DETERMINATION	METHOD	RESULT	SPECIFICATION
Peptide per vial	Calculated from fill weight and net peptide content	9.94 mg per vial labelled 10 mg, i.e. 99.4 % of label	95 to 105 % of label
Counter-ion content	Ion chromatography (cation)	Sodium 1.10 % w/w ($\pm$ 0.08 %), i.e. 0.11 mg per vial	$\leq$ 5.0 %
Trifluoroacetate	Ion chromatography, LOQ 20 ppm	Not detected	$\leq$ 1000 ppm
Water content	Coulometric Karl Fischer, USP <921>	2.80 $\pm$ 0.15 % w/w (k = 2), i.e. 0.29 mg per vial	$\leq$ 8.0 %
Mass balance	Peptide + counter-ion + water	95.40 + 1.10 + 2.80 = 99.30 % ($\pm$ 1.2 %)	Close to 100 %
pH	Potentiometric, 10 mg/ml in water	6.8	6.0 to 7.6
Solubility	Visual, 10 mg/ml and 1 mg/ml	$\geq$ 10 mg/ml in water and in bacteriostatic water; clear, colourless, free of particles within 30 s. Lipidated peptide: dissolve at pH 7.5, opalescent below pH 6	Clear solution
Bacterial endotoxins	Kinetic chromogenic LAL, USP <85>	$<$ 0.001 EU/mg ($<$ 0.01 EU per vial)	$\leq$ 10 EU/mg
Sterility	Membrane filtration, USP <71>; fluid thioglycollate 30 to 35 °C and soya bean casein digest 20 to 25 °C	No growth after 14 days, 2 vials	No growth
Residual solvents	Headspace GC, USP <467>	Acetonitrile 45 ppm; N,N-dimethylformamide, methanol, dichloromethane, diethyl ether, diisopropyl ether and piperidine each $<$ 10 ppm (LOQ 10 ppm)	ICH Q3C: acetonitrile $\leq$ 410, DMF $\leq$ 880, methanol $\leq$ 3000, dichloromethane $\leq$ 600, ethers $\leq$ 5000 ppm
Elemental impurities	ICP-MS after microwave digestion (HNO ₃ /H ₂ O ₂), USP <233>	Cd, Pb, As, Hg $<$ 0.05 μg/g; Co, V, Ni $<$ 0.10 μg/g, all below LOQ	ICH Q3D(R2) Class 1 and 2A, parenteral PDE
Chiral purity (D-amino acids)	Acid hydrolysis (6 M DCl in D ₂ O, 110 °C, 24 h), Marfey's derivatisation (FDAA), LC-MS	D-Asp 0.12 %, D-Ser 0.08 %, D-Glu 0.05 %, D-Tyr 0.04 %, others $<$ 0.05 %; alpha-methyl-Leu $<$ 0.05 %; Aib achiral; sum of D-forms 0.29 %	Each D-amino acid $\leq$ 0.2 %, sum of D-forms $\leq$ 0.5 %

Labelled 10 mg / **9.94 mg peptide** / 99.4 % of label

Labelled 10 mg; the container held 10.42 mg of powder when weighed, of which 95.4 % w/w is peptide.



SIGNATURE

NAME O. Noga

ROLE Head Laboratory Technician

DATE 2026-09-22



The sample

Sample	Retatrutide, lyophilised powder, vial labelled 10 mg
Batch number	ATRET-10-2511-01
Matrix	Research peptide
Received	2026-09-08

Identity by liquid chromatography mass spectrometry

PRINCIPLE

The sample is separated by reversed-phase chromatography and the eluent is ionised by electrospray at atmospheric pressure. Peptides ionise as a series of multiply protonated species rather than as a single ion, so the measurement is not one mass but a charge envelope, and each member of that envelope has to agree with the same neutral mass before the identification stands.

SYSTEM SUITABILITY APPLIED

CRITERION	REQUIREMENT	ACHIEVED
Mass accuracy, sample ions	within 5 ppm of theoretical	0.4 ppm
Charge states agreeing on one neutral mass	at least two	two (3+, 4+)

IDENTITY

**Deconvoluted monoisotopic mass 4728.47 Da, deviation 0.4 ppm;
observed m/z 1577.16 (3+) and 1183.13 (4+)**

Against Theoretical monoisotopic 4728.472 Da from C221H342N46O68, expected m/z 1577.165 (3+), 1183.125 (4+)

Chromatographic purity by reversed-phase HPLC

PRINCIPLE

The sample is separated on a C18 stationary phase under a water and acetonitrile gradient, both modified with trifluoroacetic acid, and the eluent is monitored by ultraviolet absorbance at 214 nanometres, where the peptide bond itself absorbs. Detection at 214 rather than 280 is deliberate: 280 sees only aromatic residues, so a peptide without tryptophan, tyrosine or phenylalanine is close to invisible at that wavelength.

SYSTEM SUITABILITY APPLIED

CRITERION	REQUIREMENT	ACHIEVED
Resolution between the main peak and its nearest neighbour	not less than 1.5	2.1 (main peak against RRT 0.97)
Tailing factor of the main peak	not more than 2.0	1.1
Theoretical plates	not fewer than 2000	79 800 (apparent, gradient)
Relative standard deviation of replicate injections	not more than 2.0 per cent	0.6 per cent, 6 injections

PURITY

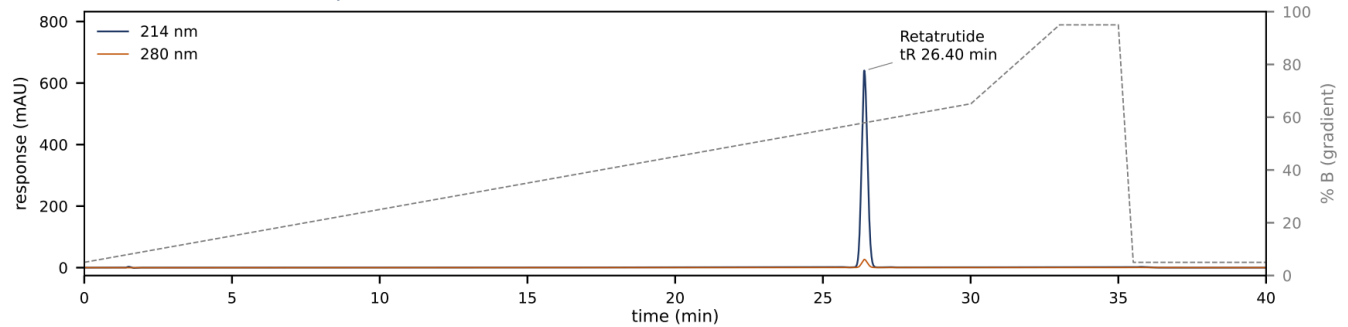
99.23 ± 0.20 % (k = 2)

Against >= 98.0 %

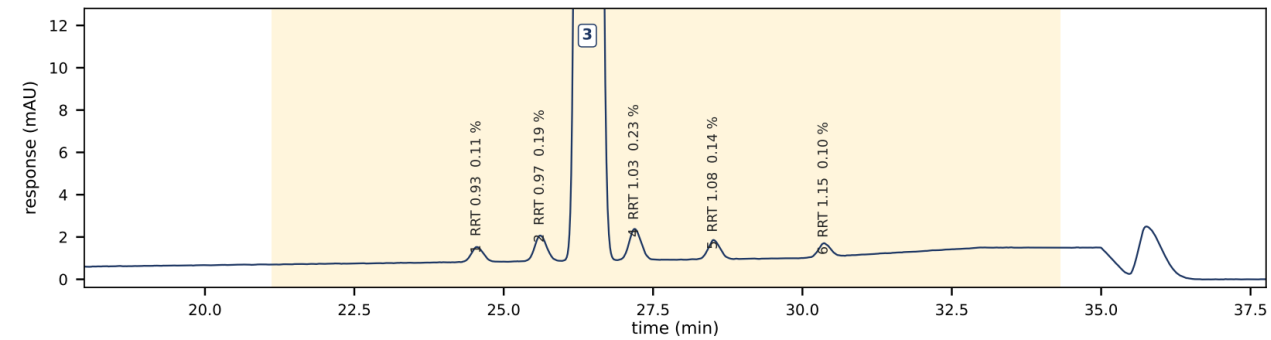
Retatrutide 10 mg · RP-HPLC purity, 214 nm

Column C18, 4.6 × 150 mm, 3 µm, 40 °C; flow 1.0 ml/min; A: 0.05 % TFA in water; B: 0.05 % TFA in acetonitrile; gradient 5 to 65 % B in 30 min, 65 to 95 % B by 33 min, 95 % B to 35 min, return to 5 % B, equilibration to 40 min; injection 10 µl, 1.0 mg/ml in water (10 µg on column).

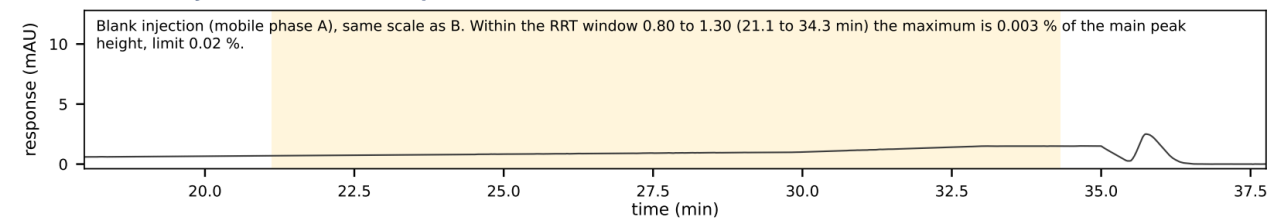
A. Full trace 0 to 40 min, full scale



B. Expanded view 0 to 2 % of the main peak height (12.8 mAU); main peak Retatrutide tR 26.40 min off scale; impurities above the 0.05 % reporting threshold, numbered as in the table; yellow band = RRT window 0.80 to 1.30



C. Blank injection before the sequence



D. Peak table and system suitability

Peak	tR (min)	RRT	Area (%)	Height (mAU)	Mass shift	Assignment
1	24.55	0.93	0.11	0.71	-18 Da	Asp succinimide/dehydration
2	25.61	0.97	0.19	1.23	same mass	Asp9 or Asp15 isomerisation to isoAsp
3	26.40	1.00	99.23	640		Retatrutide (main peak)
4	27.19	1.03	0.23	1.48	+0.98 Da	Gln3 or Gln18 deamidation
5	28.51	1.08	0.14	0.90	+16 Da	Tyr oxidation
6	30.36	1.15	0.10	0.64	-18 Da	Asp15 succinimide

Purity (main peak area of all peaks): 99.23 % · total impurities 0.77 % · largest impurity 0.23 % at RRT 1.03

System suitability (USP <621>): resolution main peak / RRT 0.97 = 2.1 (≥ 1.5); tailing factor T = 1.1 (0.8 to 1.5); theoretical plates N = 79,800 (≥ 5,000, apparent in gradient elution, peak width at half height 0.22 min); S/N at 0.03 % = 13 (≥ 10); area RSD of 6 standard injections = 0.6 % (≤ 2.0 %).

Integration: reporting threshold 0.05 %, LOD 0.01 %, LOQ 0.03 %; noise 0.030 mAU peak to peak within ± 1 min of the main peak; baseline drift 1.5 mAU over the gradient; system peaks at t0 1.5 min and at the gradient return at 35.8 min are also present in the blank and are not integrated.

Wavelength 214 nm as primary (peptide bond, also detects fragments without aromatic residues), 280 nm only as a control trace with a weak Tyr/Phe signal. Main peak 280/214 response ratio 0.041.

Water content

PRINCIPLE

Water in the sample reacts stoichiometrically with iodine generated coulometrically in the titration cell, and the charge passed gives the mass of water directly. The coulometric form is used rather than the volumetric because the quantities here are small.

SYSTEM SUITABILITY APPLIED

Cell blank drift	stable before the determination begins
Recovery of a water standard	97.5 to 102.5 per cent
Replicate agreement	within 0.2 per cent absolute

WATER CONTENT

2.80 ± 0.15 % w/w (k = 2), i.e. 0.29 mg per vial

Against <= 8.0 %

Bacterial endotoxins

PRINCIPLE

Lysate from the amoebocytes of the horseshoe crab is activated by bacterial endotoxin through a protease cascade, which cleaves a chromogenic substrate. The rate at which colour develops is proportional to endotoxin concentration, and the onset time is read against a standard curve prepared from control standard endotoxin.

SYSTEM SUITABILITY APPLIED

Standard curve correlation coefficient	not less than 0.980 in absolute value
Positive product control recovery	50 to 200 per cent
Negative control	below the lowest standard
Dilution used	at or below the maximum valid dilution

BACTERIAL ENDOTOXINS

< 0.001 EU/mg (< 0.01 EU per vial)

Against <= 10 EU/mg

Sterility

PRINCIPLE

The contents are transferred under aseptic conditions to fluid thioglycollate medium and to soya bean casein digest medium, and incubated for fourteen days at the temperatures each medium requires. Growth in either medium is a failure.

SYSTEM SUITABILITY APPLIED

CRITERION	REQUIREMENT	ACHIEVED
Incubation	not fewer than 14 days	14 days

STERILITY

No growth after 14 days, 2 vials

Against No growth

Residual solvents

PRINCIPLE

A weighed portion is equilibrated in a sealed vial and the vapour above the sample is sampled and separated by gas chromatography, with detection by mass spectrometry or flame ionisation. Sampling the headspace rather than the solution keeps involatile matrix out of the instrument.

SYSTEM SUITABILITY APPLIED

Resolution between the two closest eluting solvents	not less than 1.0
Signal to noise at the limit of quantitation	not less than 10 to 1
Repeatability of the standard	not more than 15 per cent relative standard deviation
System blank	no interfering peak at any target retention time

RESIDUAL SOLVENTS

Acetonitrile 45 ppm; N,N-dimethylformamide, methanol, dichloromethane, diethyl ether, diisopropyl ether and piperidine each < 10 ppm (LOQ 10 ppm)

Against ICH Q3C: acetonitrile <= 410, DMF <= 880, methanol <= 3000, dichloromethane <= 600, ethers <= 5000 ppm

Elemental impurities by ICP-MS

PRINCIPLE

The sample is digested in acid under microwave pressure and introduced into an argon plasma at approximately 7000 kelvin, which atomises and ionises the elements present. Ions are separated by mass to charge in a quadrupole and counted individually, which is what puts the technique at parts per billion.

SYSTEM SUITABILITY APPLIED

Internal standard recovery	80 to 120 per cent
Spike recovery in matrix	70 to 150 per cent
Calibration correlation coefficient	not less than 0.995
Digestion blank	below the reporting limit for every element
Drift check across the sequence	within 20 per cent

ELEMENTAL IMPURITIES

Cd, Pb, As, Hg < 0.05 µg/g; Co, V, Ni < 0.10 µg/g, all below LOQ

Against ICH Q3D(R2) Class 1 and 2A, parenteral PDE

Controls carried in the same sequence

Blank	Solvent blank (mobile phase A) injected before the sequence; no peak above 0.02 % of the main peak within RRT 0.80 to 1.30
Reference standard	In-house reference standard RS-RET-01 (purity 99.6 %, assigned against a primary standard, stored at -20 °C) injected at the start and end of the sequence; area difference 0.4 %, retention time within 0.1 min

Verify this certificate against the register



SCAN TO VERIFY

Scan the code, or open <https://analyton.com/verify/> and enter the report number with this key:

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The register returns every result on this report, the date of issue and the current status.

END OF REPORT

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